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OM protein - protein search, using sw model

Run on: January 16, 2003, 16:42:17, Search time: 8.21429 seconds
(without alignments)
58.517 Million cell updates/sec

Title: US-09-856-070-16

Perfected score: 25

Sequence: 1 EPEFE 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 281224 seqs, 9614412 residues

Total number of hits satisfying chosen parameters: 281224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 8%

Maximum Match 100%

Listing first 45 summaries

Database: PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	57	116083	hypothetical prote
2	25	100.0	61	A81898	hypothetical prote
3	25	100.0	62	T31625	hypothetical prote
4	25	100.0	66	T04546	hypothetical prote
5	25	100.0	80	S77762	hypothetical prote
6	25	100.0	111	T50084	hypothetical prote
7	25	100.0	123	A71836	hypothetical prote
8	25	100.0	151	A86533	small protein B11
9	25	100.0	153	S72090	small protein B11
10	25	100.0	163	S01399	H+-transporting tw
11	25	100.0	165	U01578	sugar protein T642
12	25	100.0	167	C70436	hypothetical prote
13	25	100.0	168	A11600	H+ soft Yeast prote
14	25	100.0	174	S45448	hypothetical prote
15	25	100.0	175	S48745	tropenin 1, cardia
16	25	100.0	183	S58548	H+-transporting tw
17	25	100.0	184	T07440	H+-transporting tw
18	25	100.0	187	C66433	ribosomal protein
19	25	100.0	190	C70239	conserved hypothet
20	25	100.0	195	B97350	guanylate kinase (
21	25	100.0	198	A82379	hypothetical prote
22	25	100.0	210	S55273	hypothetical prote
23	25	100.0	218	T51887	hypothetical prote
24	25	100.0	224	C78853	transcription fact
25	25	100.0	229	C56143	swf protein swin
26	25	100.0	233	T17218	hypothetical prote
27	25	100.0	237	A94441	transcription init
28	25	100.0	238	C51090	probable arylamid
29	25	100.0	243	PA0862	conserved hypothet

30	25	100.0	250	2	S48793	tropenin 1, cardia
31	25	100.0	250	4	T07902	MADS box protein -
32	25	100.0	250	2	T07100	MADS box protein h
33	25	100.0	258	2	T07217	conserved hypothet
34	25	100.0	263	2	T23473	hypothetical prote
35	25	100.0	265	2	A33513	hypothetical prote
36	25	100.0	271	2	E83942	hypothetical prote
37	25	100.0	275	2	E90425	hypothetical prote
38	25	100.0	276	2	E25345	tropenin 1, cardia
39	25	100.0	276	2	A25345	tropenin 1, cardia
40	25	100.0	284	2	A28008	tropenin 1, cardia
41	25	100.0	289	2	A44781	tropenin 1, cardia
42	25	100.0	289	2	T24475	hypothetical prote
43	25	100.0	291	2	T48617	hypothetical prote
44	25	100.0	295	2	T09725	hypothetical prote
45	25	100.0	295	2	T97326	sugar kinase, fibro

ALIGNMENTS

RESULT 1

116083

Hypothetical protein F16H11.2 - Caenorhabditis elegans

CSpecies: Caenorhabditis elegans

CDate: 20-Sep-1999 #sequence_revision 20 Sep-1999 #text_change 18-Feb-2000

CAccession: T16083

R.Wu, X.

submitted to the EMBL Data Library, April 1996

A:Description: The sequence of C. elegans cosmid F16H11.

A:Reference number: Z18458

A:Accession: T16083

A:Status: preliminary; translated from ORF/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-57 <WUX>

A:Cross-references: EMBL:U55376; NID:q1280130; PID:q1280134; PIND:AAA98006 1; GSPDR:G

A:Experimental source: strain Bristol N2; clone F16H11

C:Genetics:

A:Gene: CESP:F16H11.2

A:Map position: X

Query Match 100.0%; Score 25; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEFE 5

|||||

Db 48 EPEKE 52

RESULT 2

A81898

Hypothetical protein NMA1235 [unpublished] - Neisseria meningitidis (strain 22491 serogr

CSpecies: Neisseria meningitidis

CDate: 05-May-2000 #sequence_revision 05 May-2000 #text_change 22-Feb-2001

CAccession: A81898

K. Parkhill, S., Achtman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., MO

A. Holtby, S., Jancis, K., Leather, S., Moule, S., Mungall, K., Quail, K., Quail, M.A., Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: A01775; MIM:1922056; PMID:10761319

A:Accession: A81898

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-61 <PAK>

A:Cross-references: DB ALI6755; DB ALI6755; NID:4737342; PIND:CA84547 1; PIND:q737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA1235

Query Match 100.0%; Score 25; DB 2; Length 61;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
|||||
Db 32 EREKE 46

RESULT 3

T01625
hypothetical protein At2g18970 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F19F24.17
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19 Feb 1999 #sequence_revision 19-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01625; H84570
R:Rounsley, S.D.; Lin, X.; Kellum, K.A.; Crosby, M.L.; Brandon, E.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A:Description: Arabidopsis thaliana chromosome 11 BAC F19F24 genomic sequence.
A:Reference number: Z14153
A:Accession: T01625
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-62 <R0D>
A:Cross-references: EMBL:AF004673; NID:q3404543; PID:g3004559
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, T.P.; Fujii, J.Y.;
M.; Kuo, H.; Mollat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Mayam, L.; Taiton, L.;
cuss, D.; Nierman, W.C.; White, G.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: H84570
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <S10>
A:Cross-references: CB:AF002093; NID:g3004559; PID:g3004559; ASPDB:GN00139
C:Genetics:
A:Gene: F19F24.17; At2g18970
A:Map position: 2
A:Intons: 11/2

Query Match 100.0%; Score 25; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
|||||
Db 53 EREKE 57

RESULT 4

T04546
hypothetical protein F2g12.168 Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999
C:Accession: T04546
R:Revan, M.; Hilbert, H.; Braum, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Panteroff,
submitted to the Protein Sequence Database, February 1998
A:Reference number: Z15377
A:Accession: T04546
A:Molecule type: DNA
A:Residues: 1-66 <BEV>
A:Cross-references: EMBL:AL021710
A:Experimental source: cultivar Columbia; BAC clone F2g12
C:Genetics:
A:Map position: 4
A:Intons: 17/1
A:Note: F2g12.168

Query Match 100.0%; Score 25; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
|||||

Db 19 EREKE 23

RESULT 5

S77762
hypothetical protein M0030 - Mycoplasma capricolum (iradment)
C:Species: Mycoplasma capricolum
C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 21-Jul-2000
C:Accession: S77762; S48585
R:Bork, P.; Ouchonis, C.; Casarfi, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert,
Mol. Microbiol. 16, 955-967, 1995
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physi
A:Reference number: S77739; MUID:96059441; PMID:7476192
A:Accession: S77762
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-80 <HOR>
A:Cross-references: EMBL:Z39027; NID:q541690; PID:CAAR3706.1; PID:q4479129
A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3

Query Match 100.0%; Score 25; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
|||||
Db 46 EREKE 50

RESULT 6

T50084
hypothetical coiled-coil protein [imported] - fission yeast (Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C:Accession: T50084
R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, H.G.
submitted to the EMBL Data Library, November 1999
A:Reference number: Z25035
A:Accession: T50084
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-111 <SAU>
A:Cross-references: EMBL:AL132984; PIDN:CAH61216.1; GSPDB:GN000060; SPDB:SPAC1556.05e
A:Experimental source: strain 972h(-); cosmid c1556
C:Genetics:
A:Gene: SPDB:SPAC1556.05e
A:Map position: 1
A:Intons: 12/1, 15/2, 64/3
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YG1029w

Query Match 100.0%; Score 25; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 110+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
|||||
Db 50 EREKE 54

RESULT 7

A71836
hypothetical protein jhp1797 Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C:Accession: A71836
R:Alm, R.A.; Ling, L.S.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.;
Ives, C.; Gibson, R.; Morberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.P.
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

Journal of Management Inquiry 26(4) 399-417

Nature 392, 453-458, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70400; MIM:98166666; PMID:9537420

A:Accession: G70436
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-167 <AGP>
 A:Cross references: GB:AF000746; NID:g2983925; FIDN:AAC07183.1, FID:g2983940, GB:AE00063
 A:Experimental source: strain VF5
 A:Genetics:
 A:Gene: aq1581
 C:Superfamily: Aquifex aeolicus hypothetical protein aq1581

Query Match 100.0%; Score 25; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 73 EREKE 77

RESULT 14

AL1600
 C:Species: Listeria innocua
 C:Date: 27-Nov-2001 #sequence_revision: 27 Nov 2001 #text_change 27-Nov-2001

Reglaser, P.; Franquell, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Hernandez, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Kist, U.
 Science 294, 849-852, 2001

A:Authors: Krell, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Mak, G.; Schlueter, T.; Simoes, N.; Tierney, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.; Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MIM:21537279; PMID:11679669

A:Accession: AL1600
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-168 <GLA>
 A:Cross references: GB:AL52022; FIDN:CA95577.1; FID:g16413819; GSFDB:GN00178

A:Experimental source: strain Clp11262
 A:Genetics:
 A:Gene: lml346

Query Match 100.0%; Score 25; DB 2; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 80 EREKE 84

RESULT 14

S45548
 C:Species: Bacillus subtilis
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-Jul-2000

A:Accession: S45548; E69942
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-174 <SOR>
 A:Cross references: EMBL:109228; NID:g410114; FIDN:AAA67486.1; FID:g410130

A:Experimental source: strain Clp11262
 A:Genetics:
 A:Gene: aq1581

A:Accession: S45548
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-174 <SOR>
 A:Cross references: EMBL:109228; NID:g410114; FIDN:AAA67486.1; FID:g410130

A:Experimental source: strain Clp11262
 A:Genetics:
 A:Gene: aq1581

Leech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulle, M.; Kuchner, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma, Y.; M.; Ogawa, K.; Ohtsuka, A.; Oudega, B.; Park, S.H.; Paros, V.; Pohl, T.M.; Portete, R.; Rieder, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Sakai, T.; Seunl, A.; Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tojima, A.; Tojima, V.; Uchiya, T.; Winters, F.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Zumbstein, A.; Yoshida, A.; Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis
 A:Reference number: A69580; MIM:98044033; PMID:9484377

A:Accession: E69942
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-174 <KUN>
 A:Cross references: GB:299115; GB:AL009129; NID:g2634723; FIDN:CAA4255.1; FID:cl11855

A:Experimental source: strain 168
 A:Genetics:
 A:Gene: YpuF
 A:Start codon: TTC
 C:Superfamily: Bacillus subtilis hypothetical protein ypuF

Query Match 100.0%; Score 25; DB 2; Length 174;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 161 EREKE 165

RESULT 15

S48795
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999

C:Accession: S48795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-175 <FAR>
 A:Cross references: EMBL:X79859; NID:g587433; FIDN:CAA56239.1; FID:g587434

A:Experimental source: strain Clp11262
 A:Genetics:
 A:Gene: aq1581

Query Match 100.0%; Score 25; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
 Db 139 EREKE 143

Search completed: January 16, 2003, 16:57:46

Job time: 11:23:33 secs